

SEQUENCE LISTING

<110> Yang, Hongyuan
National University of Singapore

<120> Triacylglycerol-Deficient Fission Yeast and Its Uses

<130> 040184-000500US

<140> US 10/564,266
<141> 2006-01-09

<150> US 60/485,385
<151> 2003-07-09

<150> WO PCT/SG04/00205
<151> 2004-07-09

<160> 24

<170> PatentIn Ver. 2.1

<210> 1
<211> 25
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:PCR
amplification primer PLH1-55

<400> 1
ggggtaccac accctatttg caaca 25

<210> 2
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<223> Description of Artificial Sequence:PCR
amplification primer PLH1-53

<400> 2
ccgctcgagg aattgcttga gcagcaac 28

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amplification primer PLH1-35

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cgggatcccg acaaacgaat atgataaa 28

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 amplification primer PLH1-33

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 ggggtaccga atccatgggt agtgat 26

 <210> 6
 <211> 27
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 ccgctcgagc ccgttctata taatcgt 27

 <210> 7
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 cgggatccct tattggccta tgcaata 27

 <210> 8
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 gctctagact gaatgaatat tagtaacgc 29

<210> 9
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 amplification primer pca15

 <400> 9
 ataagaatgc ggccgcggaa gaactttgac acgtt 35

 <210> 10
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 amplification primer pca13

 <400> 10
 gctctagagg aagttggata gtgctt 26

 <210> 11
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 <212> DNA
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 <223> Description of Artificial Sequence:PCR
 amplification primer pca25

 <400> 11
 ccatcgatgt agttccatca gatatt 26

 <210> 12
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 amplification primer pca23

 <400> 12
 ccgctcgagg gtaggtagta tagttaga 28

 <210> 13
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 primer in coding region of ura4+

<400> 13
 gagaaagaat gctgagtag 19

<210> 14
 <211> 18
 <212> DNA
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<220>
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 primer in coding region of his3+

<400> 14
 gagtctttaa ttcattac 18

<210> 15
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
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 primer in region outside of flanking fragment of
 dgal+

<400> 15
 cgatagtagt caataccag 19

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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 primer in region outside of flanking fragment of
 plh1+

<400> 16
 gtatatagtagt attgcctaata 20

<210> 17
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 PLH5

<400> 17
 acgcgtcgac catggcgtct tcccaagaag a 31

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 PLH3

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 tcccccggtg taatttctag gtttatcgag 30

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 amplification primer DGA1-5

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 gggaattcca tatgtcagaa gaaacataa 29

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 amplification primer DGA1-3

 <400> 20
 tcccccggtg taggctgaca acttcaat 28

 <210> 21
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 <210> 22
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 DNA PCR amplification primer DGK3

<400> 22
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28

<210> 23
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<213> Schizosaccharomyces pombe

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<223> diacylglycerol O-acyltransferase (dgal; GeneDB
Accession No. SPCC1235.15)

<400> 23
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20 25 30
Ala Val Phe Leu His Ser Val Ser Leu Thr Leu Thr Ala Ser Trp Tyr
35 40 45
Thr Val Leu Trp Ala Phe Leu Pro Phe Trp Pro Phe Leu Ile Val Tyr
50 55 60
Leu Ile Trp Leu Ile Tyr Asp Asp Gly Phe Val Thr Gly Lys Asp Arg
65 70 75 80
Gln Lys Arg Trp Leu Arg Asn Ala Pro Pro Tyr Arg Trp Phe Cys His
85 90 95
Tyr Phe Pro Ile Arg Leu His Lys Thr Thr Glu Leu Asp Ser Glu Lys
100 105 110
Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Ile Ser Leu Gly Ala
115 120 125
Phe Gly Gly Phe Ala Ser Glu Gly Ala Asp Phe Ser Lys Leu Phe Pro
130 135 140
Gly Ile Asn Val Ser Val Leu Thr Leu Asn Ser Asn Phe Tyr Val Pro
145 150 155 160
Val Tyr Arg Asp Tyr Leu Met Ala Leu Asn Ile Asn Ser Val Ser Lys
165 170 175
Lys Ser Cys Val Ser Ile Leu Ser Arg Lys Pro Gly Asp Ser Val Leu
180 185 190
Ile Val Ile Gly Gly Ala Gln Glu Ser Leu Leu Ser Arg Pro Gly Gln
195 200 205
Asn Asn Leu Val Leu Lys Lys Arg Phe Gly Phe Val Lys Leu Ala Phe
210 215 220
Leu Thr Gly Ser Ser Leu Val Pro Cys Phe Ala Phe Gly Glu Ser Asp
225 230 235 240
Ile Phe Glu Gln Val Asp Asn Asn Pro Arg Thr Arg Ile Tyr Lys Phe
245 250 255

Gln Glu Ile Val Lys Lys Ile Ala Gly Phe Thr Val Pro Phe Phe Tyr
 260 265 270
 Gly Arg Gly Leu Leu Asn Lys Thr Phe Gly Leu Met Pro Trp Arg Lys
 275 280 285
 Pro Ile Asn Ile Val Val Gly Glu Pro Ile Asp Val Pro Lys Lys Ser
 290 295 300
 His Pro Thr Asn Gln Glu Ile Tyr Glu Val His Glu Glu Tyr Ile Arg
 305 310 315 320
 Arg Leu Glu Gly Leu Trp Asn Lys Tyr Lys Asp Val Phe Leu Pro Asn
 325 330 335
 Arg Ile Ser Glu Leu Lys Leu Ser Ala
 340 345

<210> 24
 <211> 623
 <212> PRT
 <213> Schizosaccharomyces pombe

<220>
 <223> phospholipid-diacylglycerol acyltransferase (plh1,
 GeneDB Accession No. SPBC776.14, Pombe LRO1
 Homolog 1), Lecithin:cholesterol acyltransferase

<400> 24
 Met Ala Ser Ser Lys Lys Ser Lys Thr His Lys Lys Lys Lys Glu Val
 1 5 10 15
 Lys Ser Pro Ile Asp Leu Pro Asn Ser Lys Lys Pro Thr Arg Ala Leu
 20 25 30
 Ser Glu Gln Pro Ser Ala Ser Glu Thr Gln Ser Val Ser Asn Lys Ser
 35 40 45
 Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile
 50 55 60
 Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala
 65 70 75 80
 Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser
 85 90 95
 Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe
 100 105 110
 Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly
 115 120 125
 Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser
 130 135 140
 Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu
 145 150 155 160

Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu
 165 170 175
 Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys
 180 185 190
 Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys
 195 200 205
 Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe
 210 215 220
 Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala
 225 230 235 240
 Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg
 245 250 255
 Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu
 260 265 270
 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
 275 280 285
 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
 290 295 300
 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn
 305 310 315 320
 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
 325 330 335
 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
 340 345 350
 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
 355 360 365
 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro
 370 375 380
 Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
 385 390 395 400
 Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
 405 410 415
 Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
 420 425 430
 Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala
 435 440 445
 Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
 450 455 460
 Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
 465 470 475 480

Tyr	Cys	Val	His	Gly	Val	Gly	Lys	Pro	Thr	Glu	Arg	Gly	Tyr	Tyr	Tyr	
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Thr	Asn	Asn	Pro	Glu	Gly	Gln	Pro	Val	Ile	Asp	Ser	Ser	Val	Asn	Asp	
			500					505					510			
Gly	Thr	Lys	Val	Glu	Asn	Gly	Ile	Val	Met	Asp	Asp	Gly	Asp	Gly	Thr	
		515					520					525				
Leu	Pro	Ile	Leu	Ala	Leu	Gly	Leu	Val	Cys	Asn	Lys	Val	Trp	Gln	Thr	
	530					535					540					
Lys	Arg	Phe	Asn	Pro	Ala	Asn	Thr	Ser	Ile	Thr	Asn	Tyr	Glu	Ile	Lys	
545					550					555					560	
His	Glu	Pro	Ala	Ala	Phe	Asp	Leu	Arg	Gly	Gly	Pro	Arg	Ser	Ala	Glu	
				565					570					575		
His	Val	Asp	Ile	Leu	Gly	His	Ser	Glu	Leu	Asn	Glu	Ile	Ile	Leu	Lys	
			580					585				590				
Val	Ser	Ser	Gly	His	Gly	Asp	Ser	Val	Pro	Asn	Arg	Tyr	Ile	Ser	Asp	
		595					600					605				
Ile	Gln	Glu	Ile	Ile	Asn	Glu	Ile	Asn	Leu	Asp	Lys	Pro	Arg	Asn		
	610					615					620					